

SEQUENCE LISTING



<110> Feder, John N.  
Mintier, Gabe  
Kinney, Gene G  
Ramanathan, Chandra S

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<140> US 09/932,145

<141> 2001-08-17

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<213> Homo sapiens

<400> 6  
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23

<210> 7  
<211> 1504  
<212> PRT  
<213> Homo sapiens

<220>  
<223> DATABASE ACCESSION NUMBER: Database: Genbank,  
accession number: NP\_009115

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1 5 10 15

Lys Glu Ala Arg Val Val Gly Ser Glu Leu Val Asp Thr Tyr Thr Val  
20 25 30

Tyr Ile Ile Gln Val Thr Asp Gly Ser His Glu Trp Thr Val Lys His  
35 40 45

Arg Tyr Ser Asp Phe His Asp Leu His Glu Lys Leu Val Ala Glu Arg  
50 55 60

~~Lys Ile Asp Lys Asn Leu Leu Pro Pro Lys Lys Ile Ile Gly Lys Asn~~  
65 70 75 80

Ser Arg Ser Leu Val Glu Lys Arg Glu Lys Asp Leu Glu Val Tyr Leu  
85 90 95

Gln Lys Leu Leu Ala Ala Phe Pro Gly Val Thr Pro Arg Val Leu Ala  
100 105 110

His Phe Leu His Phe His Phe Tyr Glu Ile Asn Gly Ile Thr Ala Ala  
115 120 125

Leu Ala Glu Glu Leu Phe Glu Lys Gly Glu Gln Leu Leu Gly Ala Gly  
130 135 140

Glu Val Phe Ala Ile Gly Pro Leu Gln Leu Tyr Ala Val Thr Glu Gln  
145 150 155 160

Leu Gln Gln Gly Lys Pro Thr Cys Ala Ser Gly Asp Ala Lys Thr Asp  
165 170 175

Leu Gly His Ile Leu Asp Phe Thr Cys Arg Leu Lys Tyr Leu Lys Val

180					185					190						
Ser	Gly	Thr	Glu	Gly	Pro	Phe	Gly	Thr	Ser	Asn	Ile	Gln	Glu	Gln	Leu	
195					200					205						
Leu	Pro	Phe	Asp	Leu	Ser	Ile	Phe	Lys	Ser	Leu	His	Gln	Val	Glu	Ile	
210					215					220						
Ser	His	Cys	Asp	Ala	Lys	His	Ile	Arg	Gly	Leu	Val	Ala	Ser	Lys	Pro	
225					230					235					240	
Thr	Leu	Ala	Thr	Leu	Ser	Val	Arg	Phe	Ser	Ala	Thr	Ser	Met	Lys	Glu	
245					250					255						
Val	Leu	Val	Pro	Glu	Ala	Ser	Glu	Phe	Asp	Glu	Trp	Glu	Pro	Glu	Gly	
260					265					270						
Thr	Thr	Leu	Glu	Gly	Pro	Val	Thr	Ala	Val	Ile	Pro	Thr	Trp	Gln	Ala	
275					280					285						
Leu	Thr	Thr	Leu	Asp	Leu	Ser	His	Asn	Ser	Ile	Ser	Glu	Ile	Asp	Glu	
290					295					300						
Ser	Val	Lys	Leu	Ile	Pro	Lys	Ile	Glu	Phe	Leu	Asp	Leu	Ser	His	Asn	
305					310					315					320	
Gly	Leu	Leu	Val	Val	Asp	Asn	Leu	Gln	His	Leu	Tyr	Asn	Leu	Val	His	
325					330					335						
Leu	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Ser	Leu	Glu	Gly	Leu	His	Thr	
340					345					350						
Lys	Leu	Gly	Asn	Ile	Lys	Thr	Leu	Asn	Leu	Ala	Gly	Asn	Leu	Leu	Glu	
355					360					365						
<del>Ser</del>	<del>Leu</del>	<del>Ser</del>	<del>Gly</del>	<del>Leu</del>	<del>His</del>	<del>Lys</del>	<del>Leu</del>	<del>Tyr</del>	<del>Ser</del>	<del>Leu</del>	<del>Val</del>	<del>Asn</del>	<del>Leu</del>	<del>Asp</del>	<del>Leu</del>	
370					375					380						
Arg	Asp	Asn	Arg	Ile	Glu	Gln	Met	Glu	Glu	Val	Arg	Ser	Ile	Gly	Ser	
385					390					395					400	
Leu	Pro	Cys	Leu	Glu	His	Val	Ser	Leu	Leu	Asn	Asn	Pro	Leu	Ser	Ile	
405					410					415						
Ile	Pro	Asp	Tyr	Arg	Thr	Lys	Val	Leu	Ala	Gln	Phe	Gly	Glu	Arg	Ala	
420					425					430						
Ser	Glu	Val	Cys	Leu	Asp	Asp	Thr	Val	Thr	Thr	Glu	Lys	Glu	Leu	Asp	
435					440					445						
Thr	Val	Glu	Val	Leu	Lys	Ala	Ile	Gln	Lys	Ala	Lys	Glu	Val	Lys	Ser	
450					455					460						
Lys	Leu	Ser	Asn	Pro	Glu	Lys	Lys	Gly	Gly	Glu	Asp	Ser	Arg	Leu	Ser	
465					470					475					480	
Ala	Ala	Pro	Cys	Ile	Arg	Pro	Ser	Ser	Ser	Pro	Pro	Thr	Val	Ala	Pro	

*a' cont*



785		790		795		800
His Glu Phe His	Ala Asp Leu Arg Ser Cys Phe Ala Pro Gln His Met	805		810		815
Ala Met Leu Cys Ser Pro Ile Leu Tyr Gly Ser His Thr Ser Leu Gln		820		825		830
Glu Phe Leu Arg Gln Leu Leu Thr Phe Tyr Lys Val Ala Gly Gly Cys		835		840		845
Gln Glu Arg Ser Gln Gly Cys Phe Pro Val Tyr Leu Val Tyr Ser Asp		850		855		860
Lys Arg Met Val Gln Thr Ala Ala Gly Asp Tyr Ser Gly Asn Ile Glu		865		870		875
Trp Ala Ser Cys Thr Leu Cys Ser Ala Val Arg Arg Ser Cys Cys Ala		885		890		895
Pro Ser Glu Ala Val Lys Ser Ala Ala Ile Pro Tyr Trp Leu Leu Leu		900		905		910
Thr Pro Gln His Leu Asn Val Ile Lys Ala Asp Phe Asn Pro Met Pro		915		920		925
Asn Arg Gly Thr His Asn Cys Arg Asn Arg Asn Ser Phe Lys Leu Ser		930		935		940
Arg Val Pro Leu Ser Thr Val Leu Leu Asp Pro Thr Arg Ser Cys Thr		945		950		955
Gln Pro Arg Gly Ala Phe Ala Asp Gly His Val Leu Glu Leu Leu Val		965		970		975
<del>Gly Tyr Arg Phe Val Thr Ala Ile Phe Val Leu Pro His Glu Lys Phe</del>		<del>980</del>		<del>985</del>		<del>990</del>
His Phe Leu Arg Val Tyr Asn Gln Leu Arg Ala Ser Leu Gln Asp Leu		995		1000		1005
Lys Thr Val Val Ile Ala Lys Thr Pro Gly Thr Gly Gly Ser Pro Gln		1010		1015		1020
Gly Ser Phe Ala Asp Gly Gln Pro Ala Glu Arg Arg Ala Ser Asn Asp		1025		1030		1035
Gln Arg Pro Gln Glu Val Pro Ala Glu Ala Leu Ala Pro Ala Pro Val		1045		1050		1055
Glu Val Pro Ala Pro Ala Pro Ala Ala Ala Ser Ala Ser Gly Pro Ala		1060		1065		1070
Lys Thr Pro Ala Pro Ala Glu Ala Ser Thr Ser Ala Leu Val Pro Glu		1075		1080		1085
Glu Thr Pro Val Glu Ala Pro Ala Pro Pro Pro Ala Glu Ala Pro Ala						

a'  
Cont

1090	1095	1100
Gln Tyr Pro Ser Glu His Leu Ile Gln Ala Thr Ser Glu Glu Asn Gln 1105                      1110                      1115                      1120		
Ile Pro Ser His Leu Pro Ala Cys Pro Ser Leu Arg His Val Ala Ser 1125                      1130                      1135		
Leu Arg Gly Ser Ala Ile Ile Glu Leu Phe His Ser Ser Ile Ala Glu 1140                      1145                      1150		
Val Glu Asn Glu Glu Leu Arg His Leu Met Trp Ser Ser Val Val Phe 1155                      1160                      1165		
Tyr Gln Thr Pro Gly Leu Glu Val Thr Ala Cys Val Leu Leu Ser Thr 1170                      1175                      1180		
Lys Ala Val Tyr Phe Val Leu His Asp Gly Leu Arg Arg Tyr Phe Ser 1185                      1190                      1195                      1200		
Glu Pro Leu Gln Asp Phe Trp His Gln Lys Asn Thr Asp Tyr Asn Asn 1205                      1210                      1215		
Ser Pro Phe His Ile Ser Gln Cys Phe Val Leu Lys Leu Ser Asp Leu 1220                      1225                      1230		
Gln Ser Val Asn Val Gly Leu Phe Asp Gln His Phe Arg Leu Thr Gly 1235                      1240                      1245		
Ser Thr Pro Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu 1250                      1255                      1260		
Thr His Cys Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu 1265                      1270                      1275                      1280		
<del>Arg Thr Pro Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe</del> 1285                      1290                      1295		
Gly Asn Lys Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser 1300                      1305                      1310		
Ser Arg Val Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu 1315                      1320                      1325		
Thr Phe Thr Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala 1330                      1335                      1340		
Leu Ser Ile Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro 1345                      1350                      1355                      1360		
Pro Gly Cys Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr 1365                      1370                      1375		
Ser Ser Glu Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu 1380                      1385                      1390		
Pro Glu Phe Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp		

1395

1400

1405

Asp Gly Arg Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln  
 1410 1415 1420

Thr Tyr Pro Gln Ala Leu Thr Leu Val Phe Asp Asp Val Gln Gly His  
 1425 1430 1435 1440

Asp Leu Met Gly Ser Val Thr Leu Asp His Phe Gly Glu Val Pro Gly  
 1445 1450 1455

Gly Pro Ala Arg Ala Ser Gln Gly Arg Glu Val Gln Trp Gln Val Phe  
 1460 1465 1470

Val Pro Ser Ala Glu Ser Arg Glu Lys Leu Ile Ser Leu Leu Ala Arg  
 1475 1480 1485

Gln Trp Glu Ala Leu Cys Gly Arg Glu Leu Pro Val Glu Leu Thr Gly  
 1490 1495 1500

&lt;210&gt; 8

&lt;211&gt; 100

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> OTHER INFORMATION: The nucleotide sequence is  
 nucleotides 1644 to 1743 of Incyte clone 2499870  
 DATABASE ACCESSION NUMBER: Database: Incyte,  
 Accession number: 2499870

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tacgctgtgg ccattgagttc aagccagagg agcccaggat gggattagac agtgaggaag 60  
 gctggaggcc tctgttccaa aagacagaat ctctgtctgt 100

&lt;210&gt; 9

&lt;211&gt; 100

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Other Information: The nucleotide sequence is  
 nucleotides 1794 to 1893 of Incyte clone 2499870  
 DATABASE ACCESSION NUMBER: Database: Incyte,  
 Accession number: 2499870

&lt;400&gt; 9

gaacccccaa caggagcg aaacaggag agcagtctct ggctccttct ccgtttgccca 60  
 gccctgtctg ccaccctcct ggccatggtg accaccttga 100

&lt;210&gt; 10

<211> 103  
<212> DNA  
<213> Homo sapiens

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<223> OTHER INFORMATION: The nucleotide sequence is  
nucleotides 2444 to 2546 of Incyte clone 2499870  
DATABASE ACCESSION NUMBER: Database: Incyte,  
Accession number: 2499870

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acctgcctcg tatccctggt gctgactccg tccacctgt tcc 103

<210> 11  
<211> 1289  
<212> PRT  
<213> Drosophila melanogaster

<220>  
<223> DATABASE ACCESSION NUMBER: Database: Genbank,  
Accession: AAF52305

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Gly Asp Lys Ile Leu Ser Ser Glu Phe Thr Leu Thr Leu Ser Gly Ser  
20 25 30  
Leu Leu Arg Ala Leu Asn Asp Ser Phe Thr Leu Ile Ala Asp Thr Glu  
35 40 45  
Ile Gly Thr Gly Ala Gly Tyr Leu Gln Pro Gln Ser Phe Gln Val Val  
50 55 60

Lys Pro Ile Asn Ala Lys Ser Ser Val Phe Pro Asp Leu Gln Leu Val  
65 70 75 80

His Asp Phe Val Gln Lys Thr Thr Leu Leu Lys Leu Thr Tyr Phe Pro  
85 90 95

Ser Glu His Tyr Phe Glu Gly Ala Ile Asp Ile Ala Lys Phe Arg Ala  
100 105 110

Leu Arg Arg Leu Glu Val Asn Lys Ile Asn Ile Gly Gln Val Val Gly  
115 120 125

Ile Gln Pro Leu Arg Gly Gln Leu Gln His Leu Ile Cys Val Lys Ser  
130 135 140

Leu Thr Ser Val Asp Asp Ile Ile Thr Arg Cys Gly Gly Asp Asn Ser  
145 150 155 160

Asn Gly Phe Val Trp Asn Glu Leu Lys Thr Ala Asp Phe Ser Tyr Asn  
165 170 175



Ser Leu Arg Ser Val Asp Thr Ala Leu Glu Phe Ala Gln His Leu Gln  
 180 185 190  
 His Leu Asn Leu Arg His Asn Lys Leu Thr Ser Val Ala Ala Ile Lys  
 195 200 205  
 Trp Leu Pro His Leu Lys Thr Leu Asp Leu Ser Tyr Asn Cys Leu Thr  
 210 215 220  
 His Leu Pro Gln Phe His Met Glu Ala Cys Lys Arg Leu Gln Leu Leu  
 225 230 235 240  
 Asn Ile Ser Asn Asn Tyr Val Glu Glu Leu Leu Asp Val Ala Lys Leu  
 245 250 255  
 Asp Ala Leu Tyr Asn Leu Asp Leu Ser Asp Asn Cys Leu Leu Glu His  
 260 265 270  
 Ser Gln Leu Leu Pro Leu Ser Ala Leu Met Ser Leu Ile Val Leu Asn  
 275 280 285  
 Leu Gln Gly Asn Pro Leu Ala Cys Asn Pro Lys His Arg Gln Ala Thr  
 290 295 300  
 Ala Gln Tyr Leu His Lys Asn Ser Ala Thr Val Lys Phe Val Leu Asp  
 305 310 315 320  
 Phe Glu Pro Leu Thr Lys Ala Glu Lys Ala Leu Thr Gly Ser Gln Lys  
 325 330 335  
 Trp Arg Tyr Ile Ser Gly Leu Ser His Arg Ser Pro Arg Ser Thr Ser  
 340 345 350  
 Met Ser Ile Asn Ser Ser Ser Ala Ser Ile Asn Thr Ser Asp Gly Ser  
 355 360 365  


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 Gln Phe Ser Ser Phe Gly Ser Gln Arg Ser Val Ser Ile Arg Gly Lys  
 370 375 380  
 Asn Tyr Thr Leu Glu Asp Asn Gln Ser Met Asp Thr Ser Gln Ser Ser  
 385 390 395 400  
 Lys Arg Ile Ser Ser Cys Lys Ile Arg Thr Val Asp Ile Glu Glu Ser  
 405 410 415  
 Ser Glu Ile Asn Thr Asp Ala Ala Ser Val Ser Thr Pro Asn Pro Arg  
 420 425 430  
 Ser Glu Tyr Glu Glu Glu Pro Asp Asn Ser His Leu Glu Thr Lys Lys  
 435 440 445  
 Lys Ile Glu Thr Leu Arg Leu Thr Tyr Gly Asn Glu Trp Leu Lys Ser  
 450 455 460  
 Gly Asn Ala Glu Leu Met Leu Gly Ile Glu Thr Pro Gln Pro Thr Glu  
 465 470 475 480

Arg Glu Arg Asn Glu Ser Arg Gln Leu Phe Asn Glu Tyr Leu Gly Glu  
485 490 495

Leu Ser Gly Phe Thr Glu Ala Lys Asn Asp Ser Glu His His Asn Ile  
500 505 510

Ser Ser Thr Pro Thr Asn Asn Val Leu Leu Ala Ser Thr Phe Asp Ala  
515 520 525

Thr Ile Thr Pro Ile Lys Ser Glu Ala Asn Asp Thr Ser Gly Gln Thr  
530 535 540

Leu Tyr Glu Thr Cys Thr Glu Gly Glu Glu Thr Asn Tyr Glu Ser Phe  
545 550 555 560

Gly Asn Asn Thr Thr Glu Leu Ser Thr Glu Glu Arg Pro Pro Asp Arg  
565 570 575

His Glu Glu Leu Leu Arg Leu Tyr Ala Ser Ser Ser Asn Ala Gln Asp  
580 585 590

Glu Asp Pro Val Ser Asp Ala Glu Ser Asp Glu Glu Thr Tyr Ile Val  
595 600 605

Tyr His Glu Gln Lys Pro Ser Glu Val Leu Phe Leu Thr Ile Ser Ser  
610 615 620

Asn Phe Ile Arg Glu Lys Asp Thr Leu Thr Glu Arg Thr Lys Ala Lys  
625 630 635 640

Trp Ser Leu Lys Ile Leu Glu Ser Cys Glu Arg Val Arg Ser Asn Thr  
645 650 655

Leu Arg Ile Asn Phe Asp Thr Met Arg Lys Asp Lys Gln Glu Arg Ile  
660 665 670

Tyr Cys Val Glu Asn Thr Leu Cys Gln Glu Leu Glu Lys Lys Leu Arg  
675 680 685

Asp Ile Leu Ser Gln Arg Asp Leu Thr Glu Met Asn Ile Ser Ile Tyr  
690 695 700

Arg Cys Val Asn Cys Leu Thr Gln Phe Thr Ile Glu Gln Lys Ser Lys  
705 710 715 720

Arg Tyr Lys Ala Lys Glu Leu Arg Cys Pro Asp Cys Arg Ser Val Tyr  
725 730 735

Val Ala Glu Val Thr Glu Leu Ser Ser Ser Leu Ser Lys Pro Ser Gly  
740 745 750

Glu Val Ala Ala Glu Pro Lys Leu Ser Pro Ala Met Ile Val Glu Glu  
755 760 765

Ser Pro Val Glu Glu Leu Ala Ala Ala Ile Asn Lys Glu Glu Ser Asn  
770 775 780

Ser	Ile	Gly	Lys	Ser	Leu	Ala	Ser	Phe	Leu	Phe	Tyr	Phe	Asp	Glu	Ser	785	790	795	800
Ser	Phe	Asp	Ser	Asn	Gln	Ser	Val	Val	Gly	Ser	Ser	Asn	Thr	Asp	Arg	805	810	815	
Asp	Met	Glu	Phe	Arg	Ala	Asn	Glu	Ser	Asp	Val	Asp	Ile	Ile	Ser	Asn	820	825	830	
Pro	Ser	Gln	Ser	Ser	Ile	Glu	Val	Leu	Asp	Pro	Asn	Tyr	Val	Gln	Ser	835	840	845	
Ala	Ser	Arg	Lys	Thr	Ser	Glu	Glu	Arg	Arg	Ile	Ser	Gln	Leu	Pro	His	850	855	860	
Leu	Glu	Thr	Ile	His	Asp	Glu	Val	Ala	Lys	Ser	Lys	Ser	Phe	Ile	Glu	865	870	875	880
Arg	Glu	Phe	Gly	Gln	Leu	Leu	Ala	Glu	Gln	Ala	Gln	Pro	Thr	Thr	Pro	885	890	895	
Ser	Thr	Ala	Ala	Pro	Leu	Ala	Pro	Ala	Lys	Ser	Ala	Val	Pro	Ser	His	900	905	910	
Val	Pro	Leu	Thr	Glu	Ser	Ser	Ser	Ser	Gly	Ser	Val	Thr	Asp	Ser	Ile	915	920	925	
Cys	Thr	Thr	Tyr	Glu	Gln	Gln	Ala	Thr	Asp	Ala	Pro	Gln	Asn	Leu	Gln	930	935	940	
Asn	Ser	Leu	Leu	Thr	Glu	Ser	Ser	Asn	Ser	Gln	Val	Ser	Gly	Ser	Asp	945	950	955	960
Ala	Glu	Ser	Asn	Ser	Arg	Leu	Lys	Ser	Ala	Glu	Asp	Ala	Ser	Leu	Leu	965	970	975	
Pro	Phe	Ala	Ser	Val	Phe	Gln	Ser	Thr	Asn	Leu	Leu	Met	Ser	Ser	Ser	980	985	990	
Lys	Lys	Leu	Ile	Glu	Ser	Glu	Ala	Thr	Val	Phe	Gly	Thr	Gln	Pro	Tyr	995	1000	1005	
Lys	Phe	Asn	Tyr	Ser	Asp	Phe	Asn	Asp	Ile	Asp	His	Arg	Leu	Lys	Leu	1010	1015	1020	
Tyr	Phe	Tyr	Gln	Arg	Lys	Phe	Lys	Glu	Asp	Gly	Glu	His	Phe	Lys	Trp	1025	1030	1035	1040
Leu	Ala	Lys	Gly	Arg	Ile	Tyr	Asn	Glu	Gln	Thr	Gln	Ser	Leu	Gly	Glu	1045	1050	1055	
Gly	Leu	Val	Val	Met	Ser	Asn	Cys	Lys	Cys	Tyr	Leu	Met	Glu	Ala	Phe	1060	1065	1070	
Ala	Glu	Pro	His	Asp	Asp	Val	Ala	Lys	Trp	Leu	Arg	Gln	Val	Val	Ser	1075	1080	1085	

Val Ala Val Asn Arg Leu Val Ala Ile Asp Leu Leu Pro Trp Lys Leu  
1090 1095 1100

Gly Leu Ser Phe Thr Leu Lys Asp Trp Gly Gly Phe Val Leu Leu Leu  
1105 1110 1115 1120

His Asp Met Leu Arg Thr Glu Ser Leu Leu Asn Tyr Leu Gln Gln Ile  
1125 1130 1135

Pro Leu Pro Glu Gln Cys Lys Leu Asn His Gln Pro Ser Val Thr Leu  
1140 1145 1150

Ser His Gln Trp Glu Thr Ile Ala Ser Glu Pro Val Lys Met Cys Ser  
1155 1160 1165

Leu Ile Pro Ser Cys Gln Trp Ile Cys Asp Gln Glu Lys Ser Ser Phe  
1170 1175 1180

Glu Pro Ser Leu Leu Leu Ile Thr Glu Thr His Leu Tyr Ile Ser Gly  
1185 1190 1195 1200

Asn Gly Lys Phe Ser Trp Leu Ser Asp Lys Val Gln Glu Lys Pro Ile  
1205 1210 1215

Gln Pro Glu Leu Ser Leu Asn Gln Pro Leu Ser Asn Leu Val Asp Val  
1220 1225 1230

Glu Arg Ile Thr Asp Gln Lys Tyr Ala Ile Asn Phe Ile Asp Glu Thr  
1235 1240 1245

Gln Asn Arg Cys Glu Ile Trp Lys Leu Gln Phe Glu Thr His Ala Asn  
1250 1255 1260

Ala Ala Cys Cys Leu Asn Val Ile Gly Lys Gly Trp Glu Gln Leu Phe  
1265 1270 1275 1280

Gly Val Pro Phe Ser Leu Ser Gly Thr  
1285